Software for Assessing Status of Conservation Units under Canada's Wild Salmon Policy: Instructional Manual

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Les numéros 1 à 456 de cette série ont été publiés à titre de Rapports techniques de l'Office des recherches sur les pêcheries du Canada. Les numéros 457 à 714 sont parus à titre de Rapports techniques de la Direction générale de la recherche et du développement, Service des pêches et de la mer, ministère de l'Environnement. Les numéros 715 à 924 ont été publiés à titre de Rapports techniques du Service des pêches et de la mer, ministère des Pêches et de l'Environnement. Le nom actuel de la série a été établi lors de la parution du numéro 925.

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Glossary

Benchmark: a biological reference point on metrics of status (e.g., current abundances and trends in abundance over time) that delineate three zones: Green, Amber, and Red representing increasingly depleted populations and requiring increasing management intervention.

Conservation Unit (CU): a group of wild salmon sufficiently isolated from other groups that, if lost, is very unlikely to recolonize naturally within an acceptable time frame (e.g., a human lifetime or a specified number of salmon generations).

Graphical user interface (GUI): a type of interface that allows computer users to interact with electronic media by interacting with images rather than by using text commands.

Lower benchmark: a reference point in biological status associated with significant losses in production between the Amber and Red zones, and which allows for a substantial buffer between it and any level of abundance that could lead to a CU being considered at risk of extinction by COSEWIC.

Metric: a quantifiable measure of status.

Status Zone: a zone representing the biological status of the CU delineated by biological benchmarks (Red, Amber, or Green).

Upper benchmark: (or higher benchmark) a reference point applied to biological status that is associated with harvests at the level expected to provide, on an average annual basis, the maximum catch for a CU, given existing environmental conditions.

Wild salmon: salmon that have spent their entire life cycle in the wild and originate from parents that were also produced by natural spawning and lived continuously in the wild.

ABSTRACT

Holt, C.A., and Ogden, A. 2013. Software for assessing status of Conservation Units under Canada's Wild Salmon Policy: Instructional manual. Can. Tech. Rep. Fish. Aquat. Sci. 3058: v + 43 p.

The purpose of this software package is to estimate metrics and benchmarks of biological status for Conservation Units (CUs) of Pacific salmon under Canada's Wild Salmon Policy, and to determine status in accordance with those benchmarks. The intention of this package is to promote consistency in the implementation of metrics and benchmarks recommended by Holt et al. (2009) and Holt (2012). This document provides instructions on how to use the software and assess status. Five dimensions of status are considered, based on abundances, trends in spawner abundances over time, fishing mortality relative to estimates of productivity, distribution of spawners across locations within a CU, and stock productivity. The software is Windows-based, and can be run on CUs that are data-limited by using only a subset of metrics which have relatively few data requirements (e.g., time-series of relative spawner abundances only).

RÉSUMÉ

Holt, C.A. et Ogden, A. 2013. Logiciel pour l'évaluation du statut des unités de conservation selon la Politique concernant le saumon sauvage du Canada : Manuel d'instruction. Rapp. tech. can. sci. halieut. aquat. 3058 : v + 43 p.

L'objectif de ce progiciel est d'estimer les paramètres et les données de référence concernant le statut biologique des unités de conservation (UC) du saumon du Pacifique selon la Politique concernant le saumon sauvage du Canada, et de déterminer le statut de ces UC en fonction des données de référence. Il vise à promouvoir l'uniformité dans la mise en œuvre des paramètres et des données de référence recommandés par Holt *et al.* (2009) et Holt (2012). Le document fournit des instructions sur l'utilisation du logiciel et l'évaluation du statut. Le logiciel s'intéresse à cinq dimensions du statut des UC, soit l'abondance, les tendances de l'abondance des géniteurs au fil du temps, la mortalité associée à la pêche en relation avec les estimations de productivité, la distribution des géniteurs dans les divers secteurs au sein d'une même UC, et la productivité des stocks. Le logiciel a été conçu pour Windows, et il peut être utilisé dans des UC dont les données sont limitées grâce à un sous-ensemble de paramètres qui ne nécessitent que relativement peu de données (p. ex., série chronologique de l'abondance relative des géniteurs seulement).

1. INTRODUCTION

The goal of Canada's Wild Salmon Policy (2009) is "to restore and maintain healthy and diverse salmon populations and their habitats for the benefit and enjoyment of the people of Canada in perpetuity." To accomplish this task, Conservation Units (CUs) were identified as groups "of wild salmon sufficiently isolated from other groups that, if extirpated [are] very unlikely to recolonize naturally within an acceptable timeframe...." Criteria have been developed to assess the biological status of CUs. Holt et al. (2009) suggested a multidimensional approach to status assessment that includes abundances, trends in abundance over time, distribution, and fishing mortality relative to productivity.

Benchmarks have been identified that divide status on each metric into three zones: Green, Amber, and Red, which represent increasingly depleted status, requiring increased management intervention. Benchmarks are biological reference points that relate to measurable targets or thresholds that are applied to the current abundance and/or distribution of the populations that comprise a CU, or to indicators that act as proxies for that abundance or distribution.

For each metric, Holt et al. (2009) present a number of candidate benchmarks drawn from the scientific literature, with recommendations as to which to use for Wild Salmon Policy (WSP) status assessment. Input from stock assessment staff has resulted in revisions in some benchmarks suggested by Holt et al. (2009) as documented in Holt (2012), and may result in further changes in the future. Only benchmarks recommended by Holt et al. (2009) and Holt (2012) are presented here.

1.1 Purpose and overview of software

The purpose of this software package is to estimate metrics and benchmarks of biological status for CUs, and to determine status in accordance with those benchmarks. It provides a graphical user interface (GUI) tool that will promote consistency in the application of metrics and benchmarks recommended by Holt et al. (2009) and Holt (2012) among CUs, and can be easily implemented.

In the current version of this software package (January 3, 2013) five dimensions of status are considered, those based on **abundances**, **trends** in spawner abundances over time, **fishing mortality** relative to estimates of productivity, the **distribution** of spawners across locations within a CU, and stock **productivity**. It incorporates the recommended benchmarks described by Holt et al. (2009) and Holt (2012) for the first three dimensions, with minor adjustments as noted in the documentation below. Two metrics of **distribution** are included, but benchmarks are not yet available for these metrics, and so their corresponding status is not assessed. In subsequent versions of the software, the section on distribution-based metrics could be further expanded. Two metrics of **productivity** are included with provisional benchmarks, adapted from Holt (2012).

This software package generates benchmarks for metrics of **abundance** using two methods based on a stock-recruitment relationship and three derived from habitat capacity. Benchmarks derived from the stock-recruitment relationship are estimated in two ways: the standard maximum likelihood approach that generates the most likely values for benchmarks, and a more advanced Bayesian approach that estimates the probability distribution for benchmarks and includes information on freshwater carrying capacity that is independent of the spawner and recruitment

time-series data. Model parameterization and statistical techniques are described in Holt et al. (2009) and Holt (2009). In addition, benchmarks on absolute abundances that are associated with increased risk of extirpation, derived from COSEWIC criteria, are included (Holt 2012).

The software also assesses status on temporal **trends** in spawner abundances. First, a short-term linear trend in spawner abundance is determined for the maximum of the most recent 3 generations or 10 years, using both maximum likelihood methods to estimate the most likely short-term change in abundances, and Bayesian methods to estimate the probability distribution of short-term changes. Results from the maximum likelihood analysis are compared to lower and upper benchmarks defined in Holt et al. (2009), a 25% and 15% decline in abundances, respectively. The decline estimated by the Bayesian analysis is assessed by determining the probability that it is greater than 25%. Second, long-term trends in spawner abundance are estimated from the ratio of current spawner abundance to the historical mean abundance. The benchmarks based on such ratios of means are described in Holt et al. (2009) and were adapted by Grant et al. (2011) and Holt (2012).

The third set of benchmarks and associated status assessments are estimated for **fishing mortality** relative to stock productivity. Benchmarks on this dimension can be assessed in two ways. First, they can be estimated from the parameters of a Ricker stock-recruitment relationship. Second, when stock-recruitment data are unavailable, the benchmarks may be estimated using an estimate of productivity from meta-analyses that include information from neighbouring CUs or expert judgment. The lower benchmark of F_{MSY} and the upper benchmark of $70\%F_{MSY}$ can be determined by reference to productivity estimates alone, as described in Holt et al. (2009). An additional candidate lower benchmark is included here, F_{gen} (the fishing mortality that will result in spawner abundances equal to S_{gen}, the lower benchmark on spawner abundances) which also requires an estimate of capacity (i.e., both parameters of the Ricker model). However, F_{gen} is currently not recommended as a lower benchmark.

Two metrics based on spawner spatial **distribution** are included. First, the proportion of sites with greater than 100 spawners (from the running sum over one generation) is determined over the most recent three generations or 10 years, whichever is greater (Holt et al., 2009). The second metric developed here is based on the curve described by the cumulative proportion of escapement over counting locations, ranked from most to least abundant. The area over the curve (AOC) of that relationship reflects the relative concentration of spawners among different sites within a CU; declines in the AOC values over time reflect increases in spatial heterogeneity. The AOC is based on a metric proposed by Walters and Cahoon (1985) and applied by Peacock and Holt (2012).

Finally, two metrics of **productivity** are included, based on assessments from Grant and Pestal (*in press*) and recommended by Holt (2012). The first metric is mean recruits per spawner in the current generation, with a lower benchmark at the replacement level (R/S=1). No upper benchmark is provided (Holt 2012). The second evaluates time trends in productivity as measured by residuals of the Ricker stock-recruitment function over the past two generations (Holt 2012). Provisional lower and upper benchmarks are provided derived from qualitative assessment of productivity from Grant and Pestal (*in press*) and quantitative assessment of Holtby (*in review*).

1.2 Cautions

Users should be cautious when interpreting results from this software package. In particular, careful attention should be paid to diagnostic statistics, as these will provide guidelines on the appropriate

interpretation of benchmark estimates and the resulting status assessment. The user should also carefully consider the uncertainties that are reported throughout, primarily in the text file output summaries. The software package assumes that all missing values have been infilled using suggested techniques (Holt 2010). Uncertainties in the input data are not considered here.

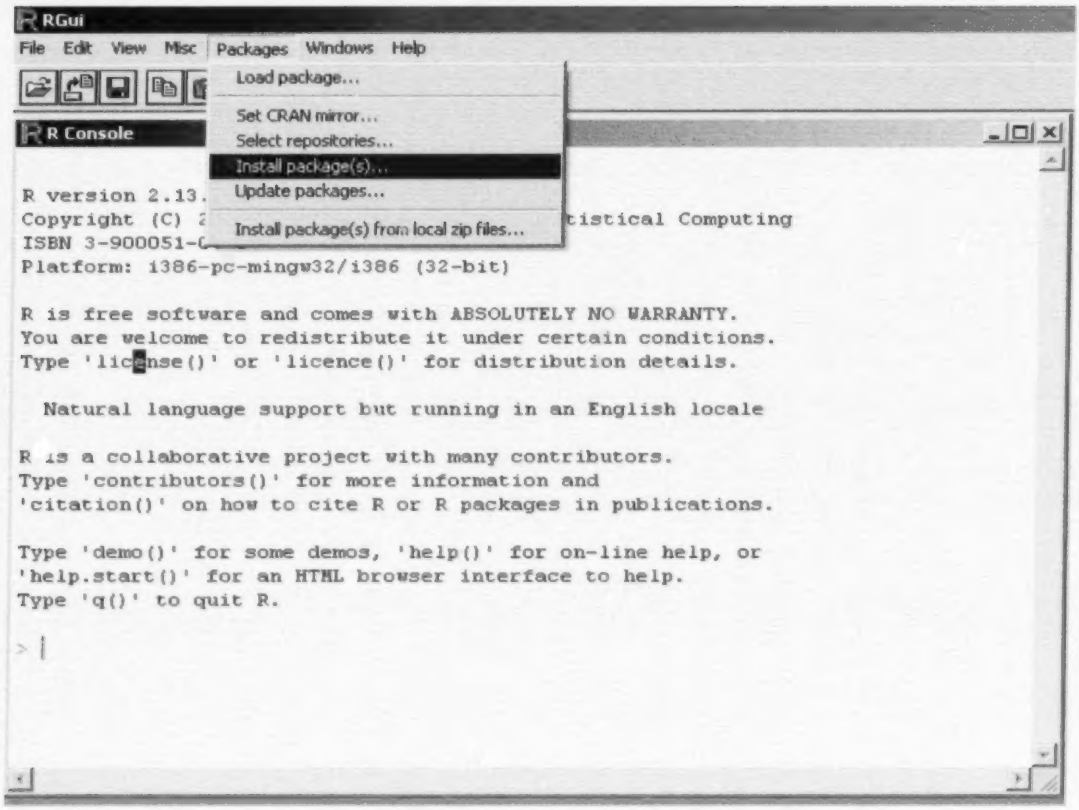
2. Starting the program

This program was built using version 2.15.2of R for Microsoft Windows, and version 2.64.236of the PBSmodelling R package. The software may not work properly under earlier versions of those statistical packages.

All of the files you will need should be available in the "BenchmarkSoftwareJan3" folder.

1) The most recent version of the R software environment is available at http://www.r-project.org/ .

2) Once the R software is downloaded, three additional statistical packages for R must be installed: coda, MCMCpack, and PBSmodelling. To do this, open the R software, go to the "Packages" menu of the R console, click on "Install package(s)," and a new window will open. You may first be asked to select a CRAN mirror site from a pop-up menu window. If so, select the site nearest you to decrease the download time. Select the first additional package to download, and click on the "OK" button. Select additional packages in the same way.


RGui
File Edit View Misc Packages Windows Help
Load package...
Set CRAN mirror...
Select repositories...
Install package(s)...
Update packages...
Install package(s) from local zip files...
R Console
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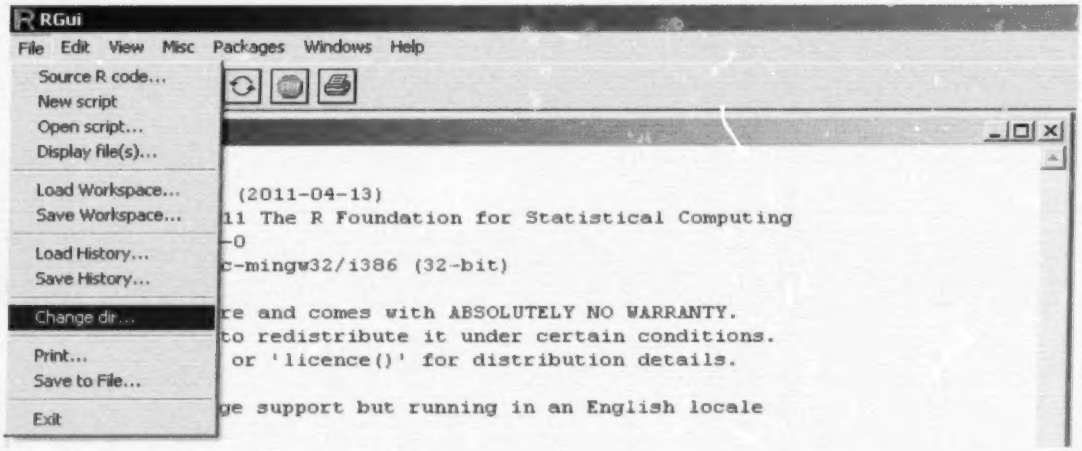
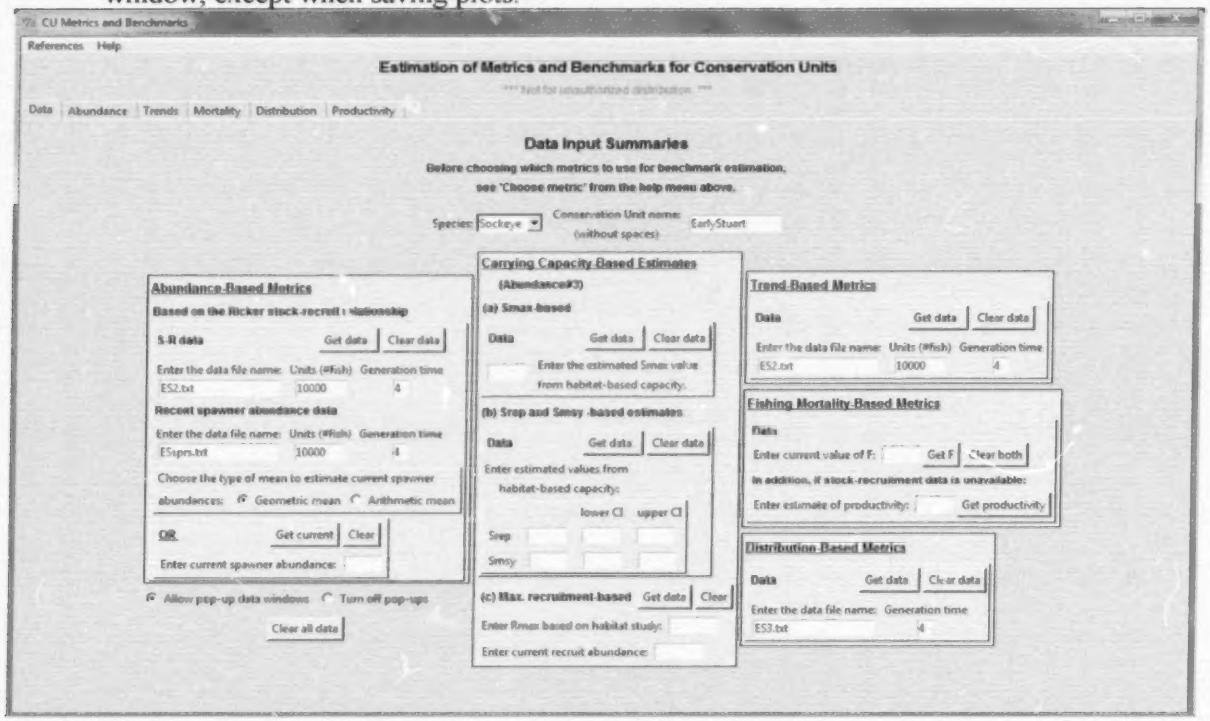
You are welcome to redistribute it under certain conditions.
Type 'license()' or 'licence()' for distribution details.
Natural language support but running in an English locale
R is a collaborative project with many contributors.
Type 'contributors()' for more information and
'citation()' on how to cite R or R packages in publications.
Type 'demo()' for some demos, 'help()' for on-line help, or
'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.
>

3) In the folder "BenchmarkSoftwareJan3," you will find the following files: "bmsMain.r," "bmsFunctions.r," "mainWin.txt," "dataWin1," "dataWin2," "dataWin3," "ES2.txt," "ESsprs.txt," and "ES3.txt." Also in BenchmarkSoftwareJan3 there is a folder called "helpFolder," which contains help and reference documents accessible from the GUI. The help folder includes the manual, "ManualJan3.doc. Save the help folder and all the files in the BenchmarkSoftwareJan3 folder, as well as your own data file(s) into a common working directory.

4) Open R in your working directory. To do this, open the R software, click "File" from the top menu of the R console, choose "Change dir..." from the drop-down menu and, from the window that appears, select the working directory where your files are located.



5) Source the file "bmsMain.r" from R. To do this, click on the "File" menu again from the top left of the RGUI and select the "Source R Code" menu item. Double-click on "bmsMain.r." A new window will open, having the title bar "CU Metrics and Benchmarks." This may take several seconds; please be patient. The first page to appear in this new window will be the **Data** page with a tab near the top of the window that you can click on to return to it at any time. The screen shot below shows the first page that will appear when you source the R file "bmsMain.r." From here, you will work exclusively from this Benchmark Estimation window, except when saving plots.


CU Metrics and Benchmarks
References Help
Estimation of Metrics and Benchmarks for Conservation Units
Data Abundance Trends Mortality Distribution Productivity
Data Input Summaries
Before choosing which metrics to use for benchmark estimation,
see 'Choose metric' from the help menu above.
Species: Sockeye
Conservation Unit name: (without spaces) EarlyStuart
Abundance-Based Metrics
Based on the Ricker stock-recruit relationship
S-R data Get data Clear data
Enter the data file name: Units (#fish) Generation time
ES2.txt 10000 4
Recent spawner abundance data
Enter the data file name: Units (#fish) Generation time
ESspn.txt 10000 4
Choose the type of mean to estimate current spawner abundances: Geometric mean Arithmetic mean
OR Get current Clear
Enter current spawner abundance:
Allow pop-up data windows Turn off pop-ups
Clear all data
Carrying Capacity-Based Estimates
(Abundance#3)
(a) Smax-based
Data Get data Clear data
Enter the estimated Smax value from habitat-based capacity:
(b) Srep and Smsy -based estimates
Data Get data Clear data
Enter estimated values from habitat-based capacity:
lower CI upper CI
Srep
Smsy
(c) Max. recruitment-based Get data Clear
Enter Rmax based on habitat study:
Enter current recruit abundance:
Trend-Based Metrics
Data Get data Clear data
Enter the data file name: Units (#fish) Generation time
ES2.txt 10000 4
Fishing Mortality-Based Metrics
Data
Enter current value of F: Get F Clear both
In addition, if stock-recruitment data is unavailable:
Enter estimate of productivity: Get productivity
Distribution-Based Metrics
Data Get data Clear data
Enter the data file name: Generation time
ES3.txt 4

The Benchmarks Estimation window cannot be resized. If it does not fit on your computer's monitor, please let the software developer know. In the meantime, you may have to use another monitor or alter the settings on your monitor's display.

Note that if it takes more than a few moments for the Benchmarks Estimation window to open, and an hourglass icon continues to show, the computer may require more RAM for the program to work efficiently. The minimum RAM required is 1.0 GB of RAM, but the program will work more efficiently, and will crash less frequently with more RAM. If the program stalls, try closing out the R GUI and reopening it by repeating the instructions above. It may also help to close any other non-essential windows. For computers that have less memory, closing and reopening R may periodically be necessary when the benchmarks estimation program stops executing.

To close the R GUI, choose "File" from the top menu of the R GUI, and select "Exit." A window will pop up, asking whether you want to save the workspace image. Click on "No." Closing the R GUI will also cause the CU Metrics and Benchmarks window to close, as well as any open, unsaved plots. The CU Metrics and Benchmarks GUI window can also be closed by clicking on the "x" in the top right edge of the window.

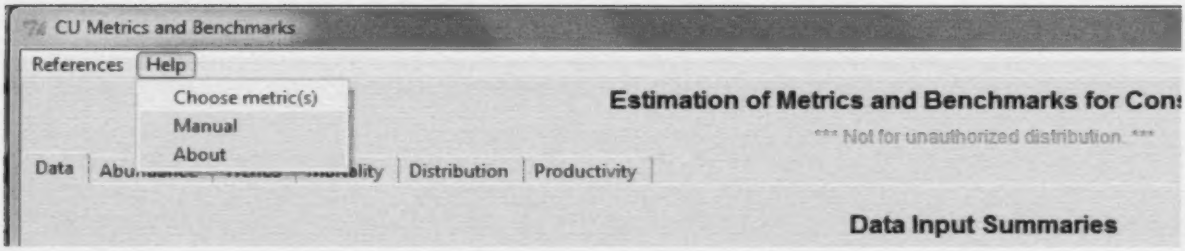
6) Proceed through the metrics and benchmark derivation and assessment pages labelled in the upper tabs and as described in the following sections. Details on data entry for metrics and the steps involved in each analysis are included in the documentation below. Redundancy in documentation among some of the different metrics pages is intentional and is meant to ensure that all information is covered if only a subset of dimensions of status is considered.

2.1 Text files

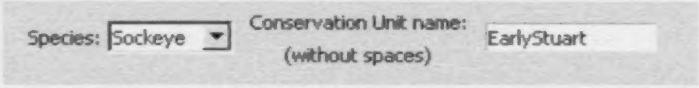
All of the outputs shown in the GUI are available in *.txt files if the user chooses to output them by clicking on "Print summary to file" on each GUI page. The output pages have been tested using Microsoft Notepad, in which the outputs line up under the appropriate headings. Some other text editors do not show the same formatting of the summary output files; all of the output data will still be present, but will not be arranged optimally.

3. Data page

The quality and quantity of data that are available will determine which metrics can be used to assess status. Please consult Table 8 from Holt et al. (2009) to determine which metrics to use depending on data availability. That table can also be found in the "Help" menu at the top of the GUI window; select "Choose metric(s)" from that drop-down menu.



1) To enter data for assessment, first select the appropriate species from the drop-down menu. Some calculations in the program will differ for pink salmon because of their short life history compared to the other Pacific salmon species.

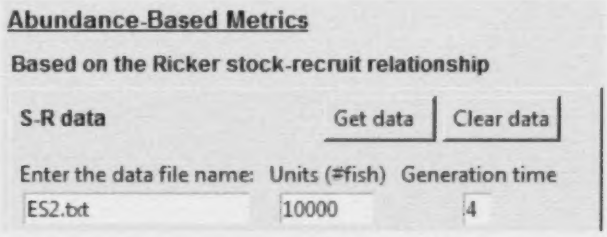


2) Enter the name of the conservation unit in the box to the right, leaving no spaces between words. The species and CU name will be used in the names of input-output summary text files. The default species and CU are sockeye salmon and EarlyStuart, respectively.

3) Note that clearing data by clicking on the "Clear Data" buttons on the **Data** page clears any associated values that may have been calculated in the metrics-determining pages. The "Clear all data" button also clears all values in the metrics pages as well as in the **Data** page.

3.1 Data for abundance-based metrics

1) Enter the name of the data file that contains spawner and recruitment time series in the box titled "Abundance-Based Metrics," under the header "Based on the Ricker stock-recruitment relationship."



The spawner-recruitment data file can have any of the following file formats: *.txt, *.r or *.dat; it must contain three columns that are separated by tabs: brood year, spawner abundances, and recruitment (both aligned by brood year), without column headers; and it must be present in the working directory. For example:

```
1950  5.9443      24.1666
1951  6.0969      17.3654
1952  3.3582      8.86
1953  15.4312     54.0891
1954  3.5058      15.5823
1955  0.2159      2.7467
```

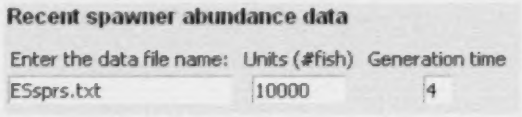
The user is responsible for making sure that there are no missing years and no rows of missing spawner or recruit data in the input data set, and that the years are sequential (or every two years for pink salmon). All values missing from the original dataset must be infilled, as suggested by Holt (2010).

If the name of a different dataset has been entered here earlier, or if the input data file has been changed, make sure to first click on "Clear data" to remove previous datasets and internal variables used for the **abundance-based metrics**, before entering the new dataset name, or click on "Clear all data," a button that appears at the bottom right of the **Data** page. Clearing data is highly recommended when switching between different datasets. Note that an example sockeye dataset "ES2.txt" has been included in the working folder and is the default data set for **Abundance-based metrics** in the software. The appropriate units for that data set are 10,000 fish (entered without a comma), and the average generation time is 4 years.

2) Enter the units (i.e., numbers of fish, entered without commas or spaces) for the abundances that apply to the values in the data file. It is important to convert the input data set to values that are between approximately 0.1 and 150, with the units adjusted appropriately. This will improve parameter optimization.

3) Enter the mean generation time in the box to the right. The value can be changed in sensitivity analyses if fish return at multiple ages-at-maturity to the CU of interest. The exception is pink salmon, for which the generation time will automatically be reset to 1 year, as there should be only 1 year of spawner return data per generation. Pink salmon that spawn in even and odd years are assessed separately under the Wild Salmon Policy.

4) Recent spawner abundances averaged over the current generation will be compared with benchmarks, and can either be calculated by the program after the user provides a time-series of spawner abundances aligned by return year as described here, or entered directly by the user (Step 6 below). To have the program do the calculation, first enter the name of another dataset that provides time-series of spawners by return year under "Recent spawner abundance data." Note that if spawner-recruit data is not available, it is possible to enter a dataset filename here without having entered a filename for the S-R data.



These data should be the most recent available escapement data, by return year, summed over populations for the entire CU. Make sure that the number of years is ≥ the entered generation time, as the generation time will be used to generate the spawner abundance value in the most recent generation. The input data file must have two columns that are separated by tabs, return year and spawner abundances; must have no column names; and must be present in the working directory. For example,

```
2004  0.9276
2005  9.8297
```

```
2006  3.5809
2007  0.5345
2008  2.9835
```

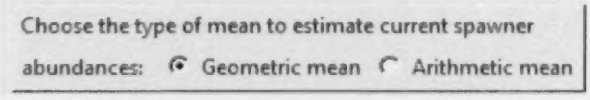
The program assumes that the units of the escapement data are the same as for the stock-recruitment data; please enter these two datasets in the same units. Units entered here will automatically change the units in the other **Abundance-based metrics** entry box for units. The generation time entered here will also alter the generation time entered earlier, if different.

For pink salmon, the current spawner abundance will be represented by the escapement in the most recent year rather than an average, and should be entered instead in the "Enter current spawner abundance" input field, as detailed below in step 6.

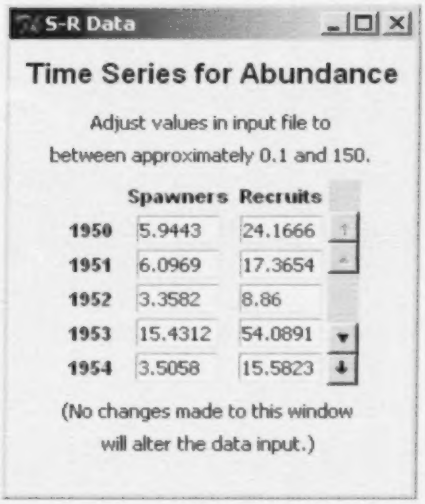
Note that an example dataset for sockeye salmon, "ESsprs.txt" has been included in the working folder and is the default dataset of escapement by return year for the software. The appropriate units for that data set are 10,000 fish (entered without a comma), and the average generation time is 4 years.

To compare abundances in the most recent year (instead of the mean of the most recent generation) to benchmarks, input the current abundance into the box to the right of "Enter current spawner abundance," as described below under step (6). As pink salmon spawner returns all occur at age 2, use this method of entry for pink salmon CUs.

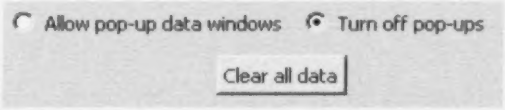
5) Select whether to use the geometric or arithmetic mean for the most recent generational mean. The geometric mean will provide a lower value and is consistent with the log-normal distribution of spawner and recruitment data; it was recommended by Holt et al. (2009) for status assessments.



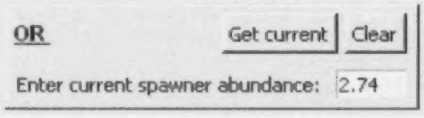
Click on "Get data" to input the data file(s) into the software. When the data are loaded, a blue window showing the S-R data will appear, which may take a moment. If only the recent spawner abundance data is entered, a blue window showing the entered data does not appear. However, the mean spawner abundance in the most recent generation is calculated as soon as "Get data" is clicked, and the current spawner abundance will appear in all of the relevant places in the **Abundance** pages #1 through #4. The data window has a scroll bar that can be used to view values anywhere in the loaded dataset. You may move or delete the data window; its only function is to allow reviewing of the input data. If you subsequently enter a different dataset, the new dataset will appear in a new window, replacing the first.



Although the data windows appear by default, it is possible to turn off the data window pop-up feature by clicking the "Turn off pop-ups" option on the bottom right of the **Data** page.



6) Current spawner abundance for the abundance-based metrics can be entered in a second way. This is how **current spawner** data should be entered for pink salmon. Beneath the generational mean selection entries is a box for entering the spawner abundance directly. Maintain the same units as the spawner-recruit data. Click on "Get current" to accept the input. Note that the value entered here will be used as the current spawner abundance for all **Abundance-based metrics** pages until cleared using the "Clear" button beside the current spawners entry box, or the "Clear all data" button on the **Data** page. The current spawner abundance entered here will appear in those pages as soon as "Get current" is clicked and will overwrite the current spawner abundance calculated from recent spawner abundance data, if a data file name was entered under "Recent spawner abundance data" for recent spawners.



The equation for the geometric mean of spawner abundance, $\overline{S_g}$, is

$$\overline{S_g} = \left(\prod_{i=1}^{n} S_i \right)^{\frac{1}{n}}$$

where S_i is the estimated annual spawner abundance in year i and n is the number of years in the generation.

7) Choose the **Abundance** tab near the top of the window to continue to the metric- and benchmark-generating pages. The analyses under the different **Abundance** tabs are independent, and they may be completed in any order. Alternatively, continue inputting data for other metrics on the **Data** page.

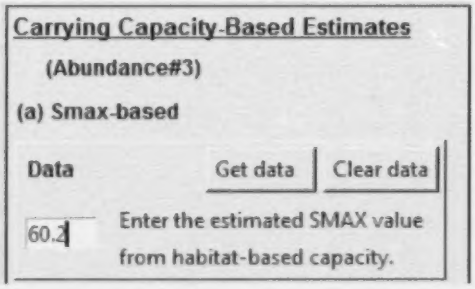
8) Note that the status assessments carried out in **Abundance** pages #1, #2, #3 a and b, and #4 depend on the data entered in the "Abundance-Based Metrics" section on the **Data** page, using "Recent spawner abundance data" or "Enter current spawner abundance."

9) Note that the COSEWIC-based **Abundance#4** status assessment page does not have its own data entry area on the **Data** page. The data required for metrics derived from COSEWIC criterion C1 are mean spawner abundances in the most current generation and short-term trends in spawner abundances (Section 3.3).

3.2 Data for carrying-capacity-based estimates

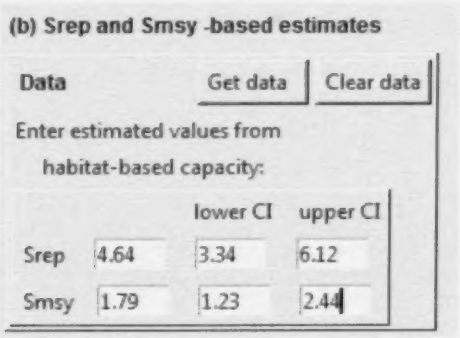
1) For benchmarks based on spawner abundances that maximum recruitment, S_{max}, spawner abundances at replacement, S_{rep}, and/or spawner abundances at maximum sustainable yield, S_{msy}, it is necessary to enter current spawner abundances as explained in points (4)-(7) in the previous section.

2) To determine benchmarks based on freshwater carrying capacity when only S_{max} is known, enter the estimated S_{max} value under "Carrying Capacity-Based Estimates." Make sure that S_{max} is in the same units as the mean current spawner abundance. The benchmarks based on the capacity will be calculated in the **Abundance#3** page.

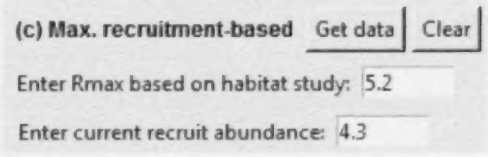


3) Click on "Get data" to accept the carrying-capacity-based S_{max}.

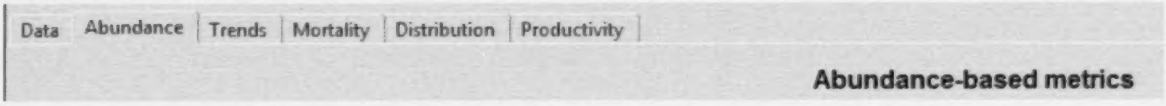
4) To determine benchmarks based on freshwater capacity when S_{rep} and S_{msy} can be estimated from accessible watershed area (Parken et al. 2006), use the "(b) S_{rep} and S_{msy}-based estimates" data entry boxes. Enter both S_{rep} and S_{msy} in the same units as the current spawner abundance. The lower and upper confidence limits of S_{rep} and/or S_{msy} may be entered if desired. Note, unlike the S_{max}-based approach in steps (2) and (3) above, using this approach, lower and upper benchmarks at S_{gen} and 80% S_{msy} will be calculated. Click "Get data."



5) To estimate status from juvenile or adult recruitment abundances, an estimate of maximum recruitment, R_{max}, is required and must be entered under "(c) Max. recruitment-based." It is also necessary to enter the recruit abundance that will be compared to benchmarks in order to determine status. Lower and upper benchmarks are provisionally set at 18% and 35% of R_{max} (Holt 2012).

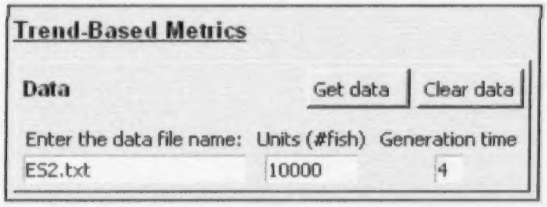


6) Choose the **Abundance** tab near the top of the window to continue to the metric- and benchmark-generating pages. Alternatively, continue inputting data for other metrics on the **Data** page.



3.3 Data for trend-based metrics

1) Enter the name of the data file in the box titled "Trend-based metrics."



The data file can be in any of the following file formats: *.txt, *.r or *.dat, and must have two columns separated by tabs, i.e., year and spawner abundances, must be present in the working directory, and must contain no column headers. For example:

```
1950  5.9443
1951  6.0969
1952  3.3582
1953  15.4312
1954  3.5058
1955  0.2159
```

The same data set may be used for both trend-based and abundance-based metrics, but the program will use only the first two columns (containing data on years and spawners) for the trend-based metrics. The user is responsible for making sure that no years are skipped in the input data set, and that the years are sequential (or every two years for pink salmon). Failing to do this will result in inaccurate status assessments on trends. All values missing from the original dataset must be infilled, as suggested by Holt (2010). Note that these spawner time series data can be aligned either by brood year (as they would be if the same dataset is used here as for the S-R abundance data) or by return year (recommended). For simplicity, the default dataset for **Trend-based metrics** is the same as that used for **Abundance-based metrics** (i.e., ES2.txt) and is aligned by brood year. Note that for the metric on long-term trends (ratio of current to historical abundances), the current spawner abundance will be calculated from the input data, and not from the current spawner abundance that may have been entered near the bottom of the **Data** page under "Abundance-Based Metrics."

If the name of a different data set has been entered here earlier, or if the input data file has been changed, make sure first to click on "Clear data" before entering the new dataset name, or on "Clear all data," a button that appears at the bottom right of the page. Clearing data is highly recommended when switching between different datasets. Note that an example dataset for sockeye salmon, "ES2.txt" has been included in the working folder and is the default dataset for **Trend-based metrics** in the software. The appropriate units for that dataset are 10000 fish, and the average generation time is 4 years.

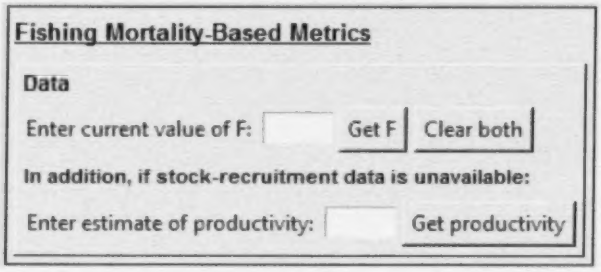
2) Enter units (i.e., numbers of fish, entered without commas or spaces) of the data and mean generation times in the cells on the right. Here, changing the units of the input dataset is not essential, but including the units if the dataset has been converted from raw values is required; otherwise, the trend of decline or increase values will be incorrect. For pink salmon, the generation time will automatically be reset to 1 year, as there should be only 1 year of data per generation. Pink salmon that spawn in even and odd years are assessed separately under the Wild Salmon Policy.

3) *Click "Get data" to input the data file into the software. A blue window will appear, similar* to the one showing the abundance-based data. It may take a moment to pop up. For properties of the data window, see the previous section (3.1), point (5).

4) Choose the **Trends** tab near the top of the window to continue to the benchmark-generating pages. The analyses under the **Trends#1** tab and **Trends#2** tab can be completed in either order.

3.4 Data for fishing mortality-based metrics

1) In the "Fishing Mortality-Based Metrics" box, enter a current value for fishing mortality (F), and click on "Get F". To use the parameters of the Ricker stock-recruitment relationship to derive benchmarks, do not enter an estimate of productivity in the estimate of productivity entry box, but make sure to have carried out one or both of the two stock-recruitment analyses in the **Abundance-based metrics** section before beginning the analyses on the **Mortality** page.



2) When productivity cannot be estimated from stock-recruitment relationships, but can be inferred from meta-analyses or nearby CUs, enter that estimate of productivity in the indicated entry box and click the "Get data" button. It is possible to generate benchmarks based on both user-derived productivity estimates, and estimates derived from the Ricker model, using maximum likelihood or Bayesian methods (i.e., one productivity estimate will not overwrite the other).

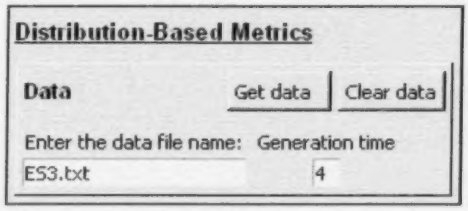
   Note that for this F-based metric, there will be no pop-up window when the data have been loaded.

3) To clear either or both data entry boxes for this metric, click on the "Clear both" button. Clearing data is recommended before entering additional values.

4) Choose the **Mortality** tab near the top of the main window to continue to the benchmark-generating pages.

3.5 Data for distribution-based metrics

1) Enter the name of the distribution data file under "Distribution-Based metrics." This file will provide a time-series of spawner abundances by counting location within the CU. If the name of a different dataset has been entered here earlier, or if the input data file has been changed, make sure to first click on "Clear data" before entering the new dataset name, or on "Clear all data," a button that appears at the bottom right of the **Data** page. Clearing data is highly recommended when switching between different datasets.



The data file can be in any of the following file formats: *.txt, *.r or *.dat, and must be present in the working directory. The data must be in columns that are separated by tabs, must have year names at the top of columns, and indices of counting location in the first column (e.g., 1, 60, 119, and 178 in the example below; character labels with punctuation are permitted, but spaces are not). It is assumed that the dataset will be presented in raw units of fish, and there is no entry for units of fish. The following is an example of the required input data format, taken from the ES3.txt data file that is included with the software package and is used as the default dataset for the distribution metric.

	1993	1994	1995	1996	1997	1998
1	-999	-999	-999	-999	78	-999
60	844	3	72	252	754	250
119	919	99	462	613	1858	349
178	1922	-999	156	792	4296	113

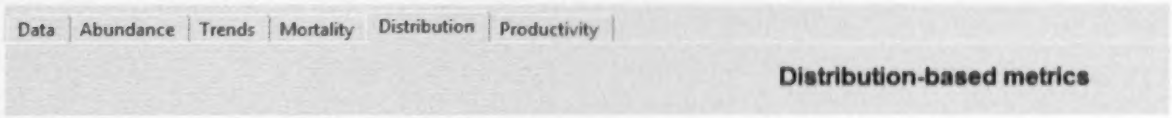
"NA" (i.e., not available) values are converted to -999 in the pop-up window. Zeroes are allowed, but should be interpreted with caution. Do not include blank cells in the input data.

Holt et al. (2009) suggest examining time trends in metrics of distribution over 3 generations. We recommend including a minimum time series of 4 generations because the running sum of spawner abundances over one generation is used to calculate metrics (except for pink salmon). However, the program can plot distribution metrics for shorter or longer time series. Note that for all species other than pink salmon, the dataset must have a minimum time series of one generation plus one year to run **Distribution-based metrics**.

2) Click "Get data" to input the data file into the software. A blue window will appear, similar to the one showing the abundance-based data. It may take a moment to pop up. For

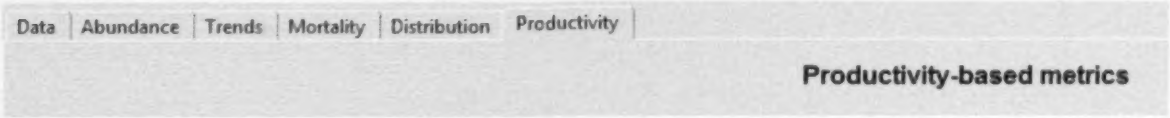
properties of the data window, see Section 3.1 at point (6). Be sure to check the data window that pops up to make sure that the data were entered as intended. NAs will appear as -999 in the data window.

3) Once the data are loaded, choose the **Distribution** tab near the top of the window to continue to the **Distribution-based metrics**.



3.6 Data for productivity-based metrics

The software also calculates provisional status based on stock productivity estimates. On the **Data** page, there is no data-entry area designed specifically for the productivity-based metrics. Instead, those metrics are based on the spawner-recruit time series data. Section 3.1 describes how to enter that data in steps (4)-(7). Once those data have been entered, choose the **Productivity** tab near the top of the window to continue to the **Productivity-based metrics**.



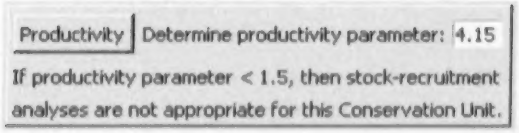
4. Abundance-based metrics

4.1 Abundance-based metrics #1: Maximum likelihood methods

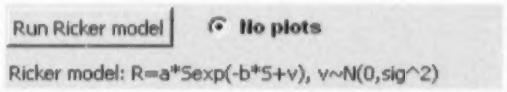
In this section, status is assessed on **abundance-based metrics** from stock-recruitment analyses using maximum likelihood methods.

1) Select the **Abundance#1** tab to go to the page that has the SRR MLE (Stock Recruitment Relationship Maximum Likelihood method for Estimation).

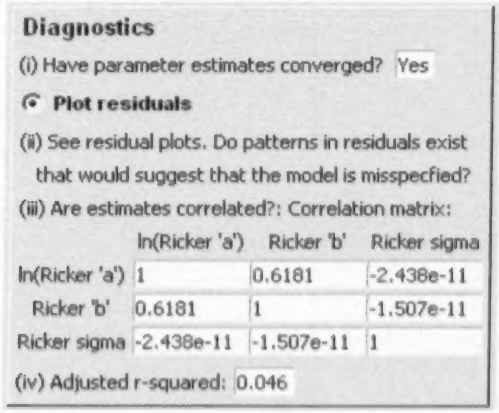
2) Prior to estimating the stock-recruitment relationship, the suitability of deriving benchmarks from those analyses is assessed by estimating the average productivity. When productivities are near or below replacement (i.e., the Ricker a parameter, or the recruits/spawner at low spawner abundances, is at or near 1), then benchmarks derived from stock-recruitment relationships are unreliable, and other methods (e.g., benchmarks derived from freshwater capacity) should be pursued. Click on the "Productivity" button to generate a rough estimate of productivity. If the value in the cell is < approximately 1.5, then benchmarks derived from stock-recruitment analyses may not be appropriate for this CU; furthermore, the optimization required for benchmark derivation may not be possible when productivity is very low.


Productivity
Determine productivity parameter: 4.15
If productivity parameter < 1.5, then stock-recruitment analyses are not appropriate for this Conservation Unit.

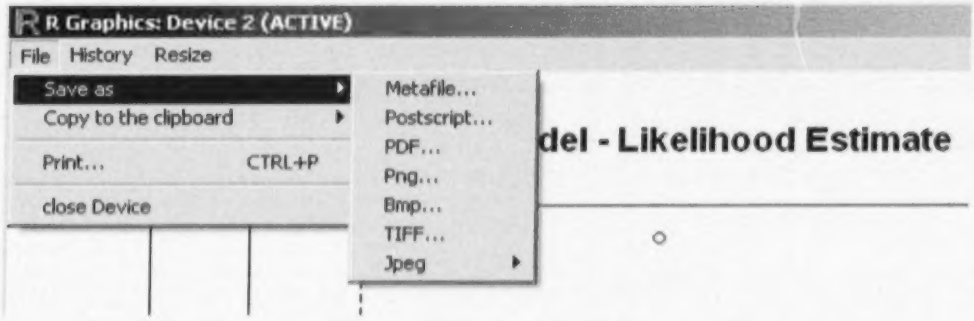
3) Click on the button "Run Ricker model." The equation of the Ricker model being used here is shown in the GUI. At present, the program does not use covariates in the stock-recruitment relationship, but they could be included in future versions of the software. The Ricker parameters will appear in the top right of the Results section. In the unlikely event that the Ricker *b* parameter is negative for the maximum likelihood estimate, the Bayesian approach to determining the parameters of the Ricker model, and the benchmarks derived from them, should be used instead of those from maximum-likelihood methods.



4) Read through the diagnostics; they will help to assess how much confidence to place in the fit of the Ricker model to the data, and therefore in the benchmarks based on that model. If the parameter estimates have not converged (item (*i*) of the diagnostics), benchmarks for abundance cannot be based on the stock-recruitment relationship for your dataset.


Diagnostics
(i) Have parameter estimates converged? Yes
Plot residuals
(ii) See residual plots. Do patterns in residuals exist that would suggest that the model is misspecfied?
(iii) Are estimates correlated?: Correlation matrix:
ln(Ricker 'a') Ricker 'b' Ricker sigma
ln(Ricker 'a') 1 0.6181 -2.438e-11
Ricker 'b' 0.6181 1 -1.507e-11
Ricker sigma -2.438e-11 -1.507e-11 1
(iv) Adjusted r-squared: 0.046

5) Select "Plot residuals" and follow the instructions in (*ii*). If the plot does not automatically pop up, click on the minimized tile at the bottom of your screen, i.e., "R Graphics: Device 2(ACTIVE)." To save a plot, select "File" from the top menu of the open graphics window, then "Save as" from the drop-down menu that appears, and choose the file format in which to save the plot.

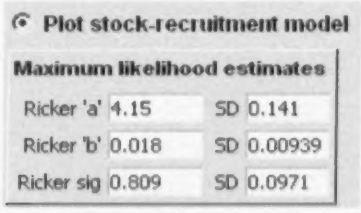


6) Next, determine the degree to which parameter estimates are correlated (*iii*). Highly correlated parameters reduce confidence in maximum likelihood estimates, and commonly occur with short time series that have poor contrast (Walters and Martel 2004). In that case, Bayesian estimates with informative prior information on freshwater carrying capacity may be more appropriate.

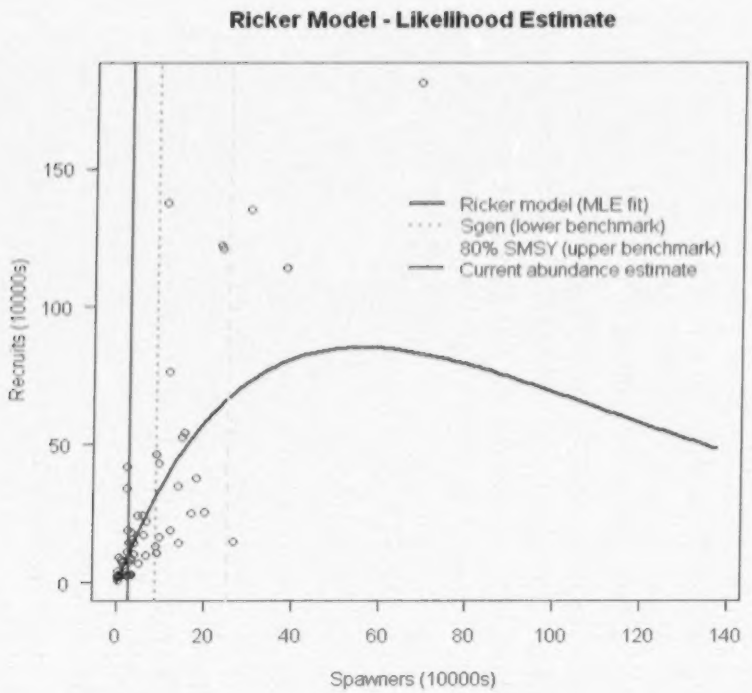
7) The adjusted r-squared (*iv*) provides a measure of the percent variance in the data that is explained by the stock-recruitment relationship.

8) After reviewing the diagnostics, proceed to the Results section.

9) Plot the Ricker stock-recruitment model by selecting that option. That selection will also generate the estimates of the Ricker parameters.


Plot stock-recruitment model
Maximum likelihood estimates
Ricker 'a' 4.15 SD 0.141
Ricker 'b' 0.018 SD 0.00939
Ricker sig 0.809 SD 0.0971

The plot will show the Ricker model fit, the estimate of current spawner abundance, and the upper (80% of S_{MSY}) and lower (S_{gen}) benchmarks derived from the stock-recruitment relationship.



Benchmarks are estimated from the maximum likelihood estimates of the Ricker parameters. Status will be indicated with an "x" in one of the coloured entry boxes. The values shown are in the same units as the input data.

Current spawner abundance	2.74
Derived parameters from Ricker	
Spawners at max recruitment	55.708
Sgen (lower benchmark)	8.9902
80% of SMSY (upper benchmark)	25.386
Corresponding status	x

10) Enter any notes in the text entry box to be included in the output summary file. The program will accept multiple lines of notes, with or without hard returns.

Enter notes to include in the output file:

```
1972 escapement from BY is mean of 1971 and 1973
```

Print summary to file

11) Click on "Print summary to file" to generate a text file with all of the inputs and outputs shown on the page. The file will be saved in the working directory, and is named according

to the species and CU name that was entered on the **Data** page, and the metric that was summarized. For example, "SE_EarlyStuart_Abund1.txt" is the name of the summary file that summarizes the **Abundance-based metrics #1** analysis for Sockeye (SE), where the user entered "EarlyStuart" as the CU name.

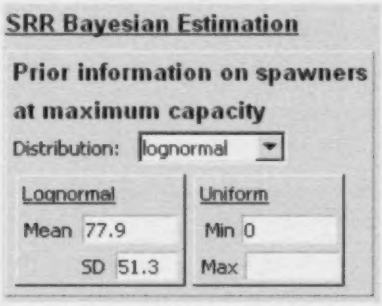
4.2 Abundance-based metrics #2: Bayesian methods

In this section, the user is guided through the assessment of status for **abundance-based metrics** derived from a stock-recruitment relationship, using Bayesian methods that explicitly include information on habitat capacity, which is in the form of a prior probability distribution. Users must specify the form and parameters of the prior probability distribution on habitat capacity. The Bayesian analysis uses Monte Carlo Markov Chain (MCMC) iterations to approximate the posterior probability of the parameters of the stock-recruitment relationship.

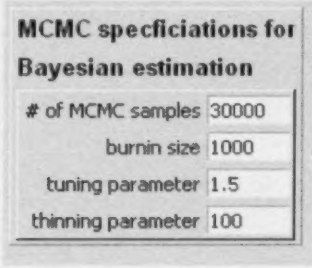
1) Click on the tab labelled **Abundance#2**.

2) Note that if data are very uninformative, then benchmarks based on Bayesian methods may be unreliable or might not be estimable. Uninformative data include data that are comprised of short time series and/or are lacking contrasts in spawner abundances.

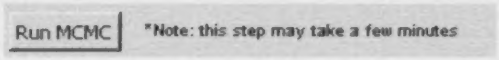
3) From the drop-down menu under "SRR Bayesian Estimation," choose a distribution for the prior distribution (lognormal or uniform) and enter the parameter values for the distribution in the appropriate entry boxes below it. For the lognormal prior distribution, the mean and standard deviation (SD) are input in raw values (i.e., number of fish, in units specified on the **Data** page).



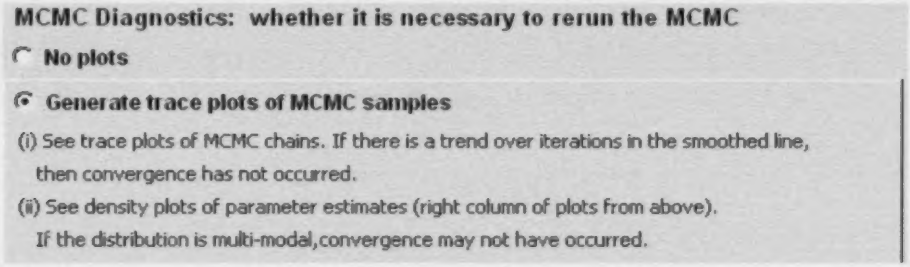
4) Choose the MCMC specifications in the box to the right. Default values are provided, but adjustments may be needed for different datasets. For more details, see instructions under "MCMC Diagnostics" in the GUI itself, and in the documentation below.

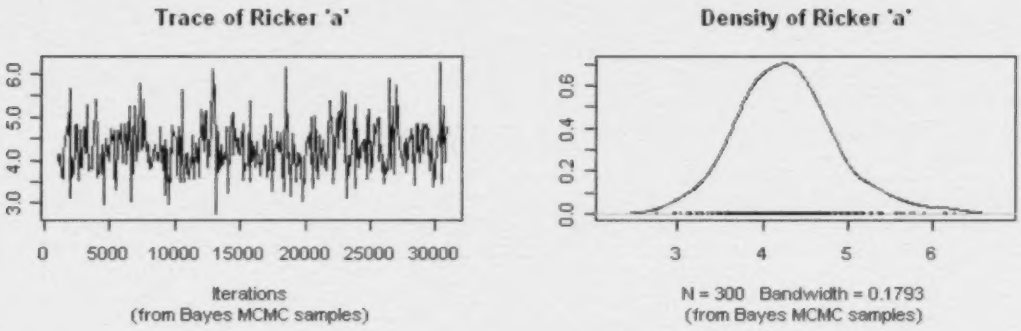


5) To start the Bayesian analysis, click on the "Run MCMC" button. This step will take a few moments. When the iterations are finished, the button will appear to "pop" back up.



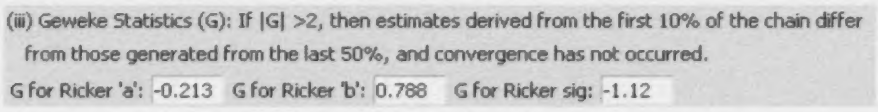
6) Next, assess MCMC diagnostics to determine whether convergence of parameter estimates has occurred and whether it is necessary to rerun the MCMC chain with different MCMC specifications. To do this, first select "Generate trace plots of MCMC samples" and read through the instructions (*i*) and (*ii*) in the GUI window.


MCMC Diagnostics: whether it is necessary to rerun the MCMC
No plots
Generate trace plots of MCMC samples
(i) See trace plots of MCMC chains. If there is a trend over iterations in the smoothed line, then convergence has not occurred.
(ii) See density plots of parameter estimates (right column of plots from above). If the distribution is multi-modal,convergence may not have occurred.


Trace of Ricker 'a'
3.0 4.0 5.0 6.0
0 5000 10000 15000 20000 25000 30000
Iterations
(from Bayes MCMC samples)
Density of Ricker 'a'
0.0 0.2 0.4 0.6
3 4 5 6
N = 300 Bandwidth = 0.1793
(from Bayes MCMC samples)

The figure directly above shows the trace plot of MCMC iterations for the Ricker *a* parameter on the left, showing no obvious trends over time. The figure on the right shows the posterior density function for the Ricker *a* parameter, which is unimodal.

7) Next evaluate the Geweke statistics as described in step (*iii*).


(iii) Geweke Statistics (G): If |G| >2, then estimates derived from the first 10% of the chain differ from those generated from the last 50%, and convergence has not occurred.
G for Ricker 'a': -0.213
G for Ricker 'b': 0.788
G for Ricker sig: -1.12

8) Select "Generate autocorrelation plots" to evaluate autocorrelation in MCMC iterations of parameter estimates, as described in step (*iv*).

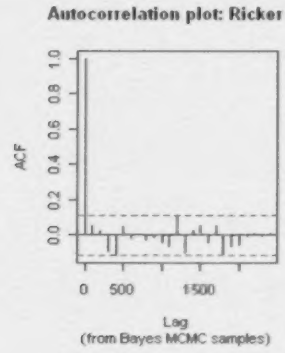
Generate autocorrelation plots

(iv) See autocorrelation plots. If MCMC iterations are autocorrelated at >1 lag (i.e., the bars are > blue dashed lines), the chain is autocorrelated and the thinning parameter should be increased.

9) If convergence in parameter estimates is not achieved as indicated by the diagnostics described above, then parameter estimates will be unreliable; the MCMC specifications should be adjusted and the Bayesian analysis re-run.

   a. If the trace plots show a non-linear trend at the start of the iterations, if the density function is multimodal, or if the Geweke statistic is greater than the absolute value of 2, then the burn-in size may need to be increased, the number of MCMC trials increased, or the tuning parameter increased or decreased (between 1 and 4).

   b. If the autocorrelation plots show significant autocorrelation, then both the thinning parameter and the number of MCMC iterations should be adjusted upwards.

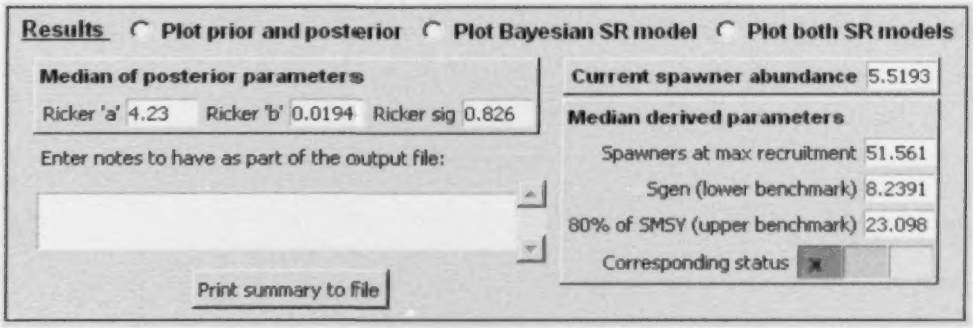


The figure above shows an uncorrelated autocorrelation plot for the Ricker *a* parameter. Although the first bar extends above the blue dashed line, it can be ignored.

10) Once the MCMC iterations have converged, click on "Show results," and proceed to the Results box at the bottom of the window.

Show results | If convergence is successful, show results.

11) Select "Plot prior and posterior" to plot the prior distribution of spawners at maximum capacity specified by the user and the posterior distribution generated by the Bayesian analysis.


Results
Plot prior and posterior
Plot Bayesian SR model
Plot both SR models
Median of posterior parameters
Ricker 'a' 4.23
Ricker 'b' 0.0194
Ricker sig 0.826
Enter notes to have as part of the output file:
Print summary to file
Current spawner abundance 5.5193
Median derived parameters
Spawners at max recruitment 51.561
Sgen (lower benchmark) 8.2391
80% of SMSY (upper benchmark) 23.098
Corresponding status

Click on "Plot Bayesian SR model" to plot the stock-recruitment model that uses the Bayesian parameter estimates and the benchmarks estimated from that model. The plot will usually be very similar to the Ricker MLE graph shown earlier. To compare the benchmarks from both the maximum likelihood and Bayesian analyses, check "Plot both SR models." The Ricker MLE values will appear on the latter plot only if they were generated on the **Abundance-based metrics #1** page.

12) The box to the right shows the median estimates of the upper and lower benchmarks from the Bayesian analysis as suggested by Holt et al. (2009). The current spawner abundance is shown with the corresponding status relative to those benchmarks at the bottom. The units are the same as for the original data.

13) Enter any notes in the text box to be included in the output summary file.

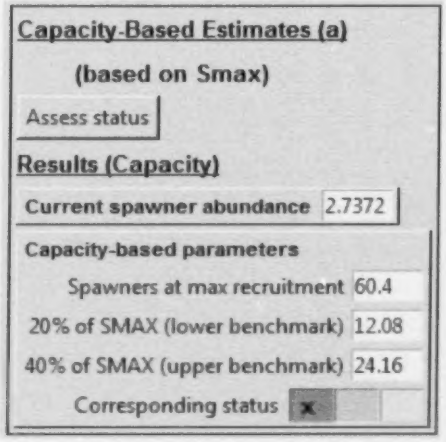
14) Click on "Print summary to file" to generate a text file with all of the inputs and outputs shown on the page, as well as the 10^{th}, 25^{th}, 50^{th}, 75^{th}, and 90^{th} percentiles of the posterior probability distributions for all of the derived parameters. The output file will be saved in the working directory, named according to the species and CU name that was entered on the **Data** page, and the metric that was summarized, as detailed at the end of section 4.1.

4.3 Abundance-based metrics #3: Habitat capacity-based methods

In this section, status is assessed separately on **abundance-based metrics** using three different methods for estimating abundance from habitat capacity data (Holt et al. 2009; Holt 2012). Status assessment based on carrying-capacity (a) through (c) are determined on the **Abundance#3** page. They can be completed in any order, and subsets of the status assessments may be completed.

1) First enter current spawner abundance or data from which to calculate it on the **Data** page under "Abundance-Based Metrics."

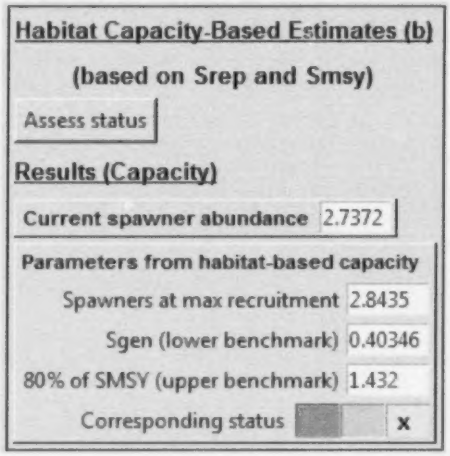
2) If the S_{max}-based capacity estimate (a) was entered on the **Data** page, click on the button "Assess status" to generate the capacity-based outputs and benchmarks in the box for "Capacity-Based Estimates (a)."



The same current spawner estimate (i.e., mean spawners in the last generation) is used for comparison in estimates based on S_{max}, and on S_{rep} and S_{msy}, and it will appear as soon as "Get data" or "Get current" is clicked on the **Data** page in the "Abundance-Based Metrics" section.

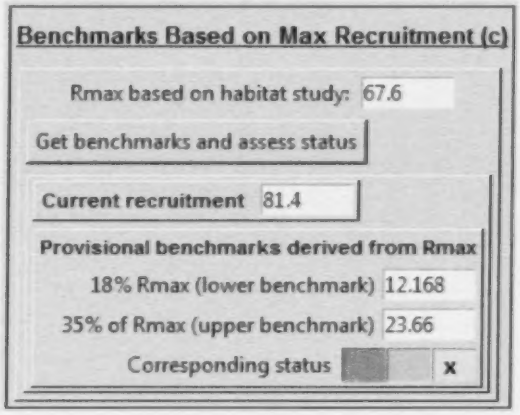
Upper and lower benchmarks are estimated as 20% and 40% of the S_{max} value entered in the **Data** page. Status will be indicated with an "x" in one of the coloured entry boxes. The values shown are in the same units as the input data.

3) Status based on capacity-based estimates of S_{rep} and S_{msy} (Parken et al. 2006) is determined under "Habitat Capacity-Based Estimates (b)." Again, current spawner abundance or data from which to calculate it must first be entered on the **Data** page under "Abundance-Based Metrics," and the current spawner abundance will appear here as soon as the "Get data" or "Get current" button is clicked on the **Data** page. If the S_{rep} and S_{msy}-based estimates (b) were entered in the **Data** page, click on "Assess status" here.



Here the lower benchmark is S_{gen} and the upper benchmark is 80% of S_{msy}. Status will be indicated with an "x" in one of the coloured entry boxes. The values shown are in the same units as the input data.

4) If R_{max} and current recruit abundances have been entered on the **Data** page under "(c) Max. recruitment-based," status can be assessed under "Benchmarks Based on Max Recruitment (c)." Note, the provisional lower and upper benchmarks used for determining status (18% and 35% of R_{max}, respectively) are approximately equal to 40% and 80% of S_{msy}, respectively, for moderate productivity CUs (Ricker a ~2.7), but will overestimate 40% and 80% of S_{msy} when productivity is low (< 1.6) or high (> 4.4) (i.e., will be more precautionary) (Holt 2012). Click on "Get benchmarks and assess status."


Benchmarks Based on Max Recruitment (c)
Rmax based on habitat study: 67.6
Get benchmarks and assess status
Current recruitment 81.4
Provisional benchmarks derived from Rmax
18% Rmax (lower benchmark) 12.168
35% of Rmax (upper benchmark) 23.66
Corresponding status
x

Status will be indicated with an "x" in one of the coloured entry boxes. Although this metric was initially intended for application to juvenile recruitment data, assuming density-dependent survival in freshwater and a linear relationship between smolt abundances and adult recruits, benchmarks on adult recruits may also be considered (Holt 2012).

5) Once all the desired capacity-based status assessments have been made, enter any notes in the text entry box to be included in the output summary file. The program will accept multiple lines of notes, with or without hard returns.

6) Click on "Print summary to file" to generate a text file with all of the inputs and outputs shown on the page. The file will be saved in the working directory, named by the species and CU name that was entered on the **Data** page, and the metric that was summarized, as detailed at the end of section 4.1. E.g., SE_EarlyStuart_Abund3.txt.

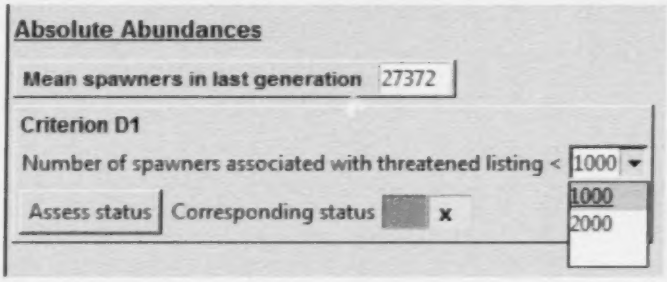
4.4 Abundance-based metrics #4: COSEWIC-based methods

In this section, status is assessed based on two COSEWIC-based metrics. Red status is assigned when status would result in a COSEWIC threatened listing. Green status is assigned if status is higher (i.e., does not result in a COSEWIC threatened or endangered listing). Amber status is not assigned here.

(1) First enter data in the **Data** page under "Abundance-Based Metrics" to obtain a current spawner abundance estimate. If the entry is made under "Recent spawner abundance data," the program will automatically convert the numbers using the given units. If the "Get current" entry method is used instead, keep the current spawner abundance as the raw number (i.e., without converting into the same units as the S-R data or recent spawner abundance data).

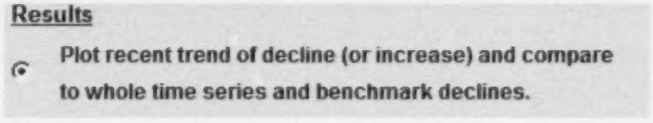
(2) Click on the tab labelled **Abundance#4.**

(3) COSEWIC criterion D1 defines "threatened" status as having a total of <1,000 mature individuals in the Canadian population. Here, the user has the option of choosing either 1,000 (the default) or 2,000 spawners from a drop-down menu, to be used as the lower benchmark.



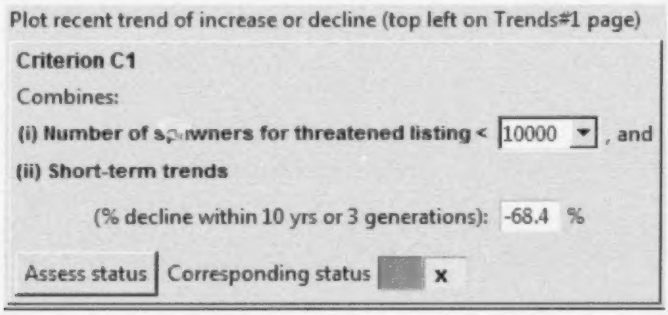
4) Click on "Assess status," which will cause the mean spawners in the last generation to appear in the correct units for comparison to the spawner number associated with the COSEWIC threatened listing. This value is based on the data entered in the "Abundance-Based Metrics" section on the **Data** page. To enter a the number of spawners from a single year instead of having the program calculate the mean of the last generation, simply enter the desired spawner number for comparison in the "Enter current spawner abundance" entry box on the bottom left of the **Data** page. An "x" will appear in the appropriate status box. Note that there are only Red and Green status zone assignments, based on the single benchmark used here.

5) COSEWIC Criterion C1 defines threatened status as a population decline of 10% within the longer of 10 years or three generations, combined with total number of mature individuals <10,000. Because part of the status assessment involves population decline, the user must first plot the recent trend of decline or increase on the **Trends#1** tab, on the **Trends** page. This requires first obtaining the data for trends from the **Data** page as detailed in Section 3.3. Then click on "Plot recent trend..." on the **Trends#1** page.



6) Once "Plot recent trend..." has been selected on the **Abundance#3** page, the % population decline (if negative) or % increase (if positive) will appear. Again, the drop-down menu

allows the user to select the default COSEWIC benchmark of 10,000 or 15,000 as the benchmark to be used.


Plot recent trend of increase or decline (top left on Trends#1 page)
Criterion C1
Combines:
(i) Number of spawners for threatened listing < 10000 , and
(ii) Short-term trends
(% decline within 10 yrs or 3 generations): -68.4 %
Assess status
Corresponding status
x

7) Clicking on "Assess status" in the Criterion C1 box will automatically show mean spawners for the most recent generation, if it has not already been generated by clicking "Assess status" for COSEWIC Criterion D1. An "x" will appear, indicating status based on those values. Again, there are only Red and Green status zone assignments, based on the combined single benchmark used here.

8) Enter any notes in the text entry box to be included in the output summary file. The program will accept multiple lines of notes, with or without hard returns.

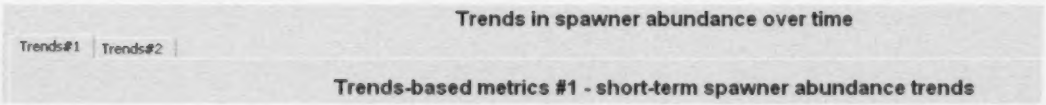
9) Click on "Print summary to file" to generate a text file with all of the inputs and outputs shown on the page. The file will be saved in the working directory, named by the species and CU name that was entered on the **Data** page, and the metric that was summarized, as detailed at the end of section 4.1., e.g., SE_EarlyStuart_Abund4.txt.

5. Trends-based metrics

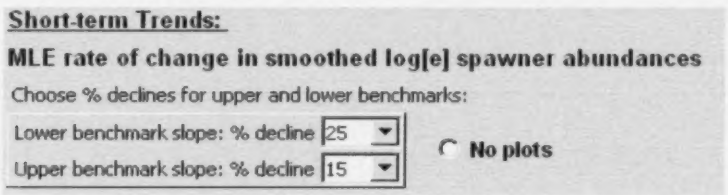
5.1 Trend-based metrics #1: Short-term trends in spawner abundance

In this section, status on short-term trends in spawner abundances is assessed in two ways. First, maximum likelihood estimation (MLE) is used to estimate the recent percent decline in spawner abundances over the longer of 10 years or 3 generations derived from best fit line of the smoothed, log-transformed abundances. Second, Bayesian analyses are used to estimate the posterior probability distribution of the same recent decline. The probability that the current short-term trend is a decline of magnitude greater than 25% is assessed. The prior probability distribution of the short-term decline in spawner abundances is assumed to follow a uniform distribution (i.e., to be relatively uninformative) with a range specified by the user.

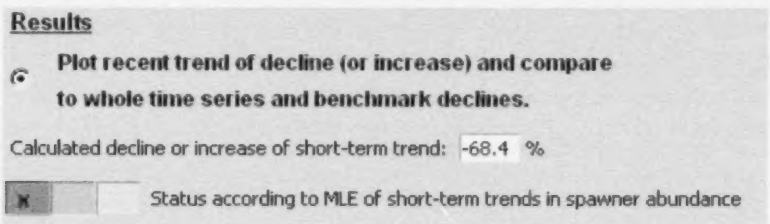
1) Select the **Trends#1** tab to assess short-term trends in spawner abundance. The maximum likelihood estimation (MLE) of the rate of change in the smoothed spawner abundances must be completed before the Bayesian (MCMC) assessment. Smoothed abundances in year t are calculated as the arithmetic mean of logged abundances for year t-(generation length-2) to t+1. Other smoothing windows may be considered in future versions of the software.

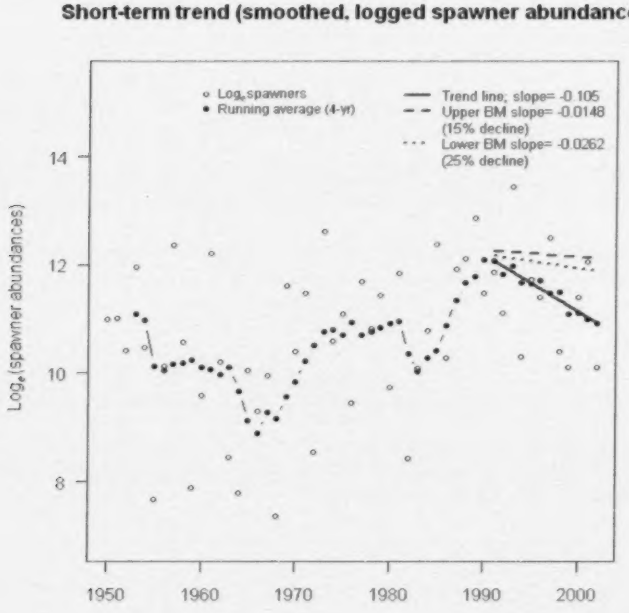


2) The default lower and upper benchmarks are set at a decline in spawner abundances of 25% and 15% over the longer of 3 generations or 10 years (Holt et al., 2009). It is possible to adjust those default benchmarks if required.

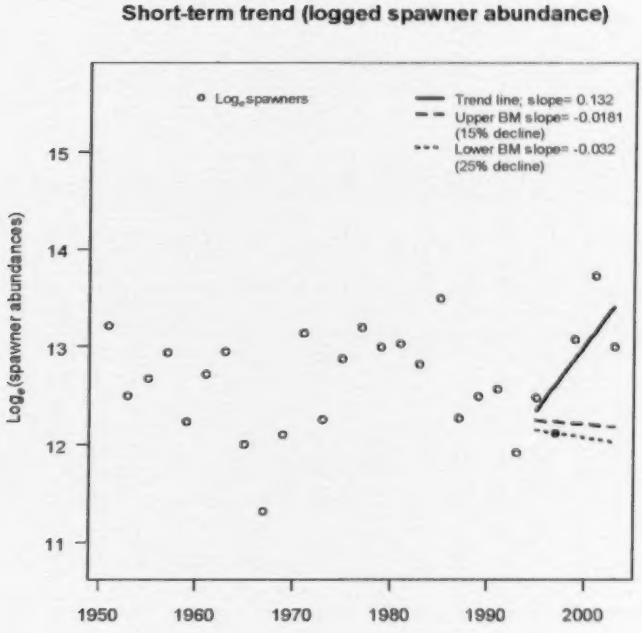

Short-term Trends:
MLE rate of change in smoothed log[e] spawner abundances
Choose % declines for upper and lower benchmarks:
Lower benchmark slope: % decline 25
Upper benchmark slope: % decline 15
No plots

3) Select "Plot recent trend of decline..." to generate a graph of the linear trend in spawner abundances over the last 10 years or 3 generations, and to determine the status based on that trend. To save a plot, or if the plot does not immediately appear, follow the directions given in Section 4.1. The maximum-likelihood estimate of the short-term trend (transformed to percentage change of raw [i.e., non-logged] numbers of fish) is also shown.

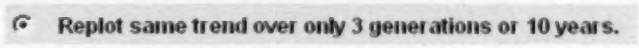

Results
Plot recent trend of decline (or increase) and compare to whole time series and benchmark declines.
Calculated decline or increase of short-term trend: -68.4 %
Status according to MLE of short-term trends in spawner abundance



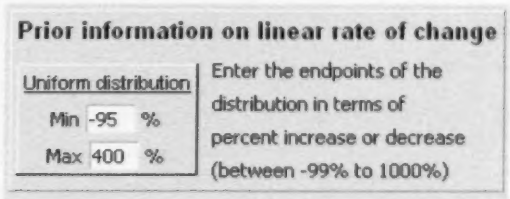
The figure directly above shows the $\log_e$-transformed spawner abundances (open circles) and the smoothed (the one-generation running average) of the logged spawner abundances (filled circles). The upper benchmark decline of 15% converted into the natural logarithm (dashed line) is shown, as well as the lower (25% decline) benchmark (dotted line). Both the natural logarithm of the absolute decline and the natural logarithm of the upper and lower benchmarks (noted in legend) will vary with the number of years included in the average generation time (entered on the **Data** page). The thick solid line in the figure shows the estimated linear decline, fit to the last three generations (12 years in this example) of smoothed, logged spawner abundance (Holt et al. 2009). For pink salmon, smoothed abundances will not be shown (see next figure for an example).



To generate a plot of only the last 10 years or 3 generations, showing the trend over those years and the benchmark decline trend lines, click on the appropriate selection:



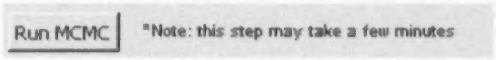
4) To estimate the probability distribution of short-term linear trends, enter the range of the uniform distribution of the prior probability on the percent decline in spawner abundances over the longer of 10 years and 3 generations (automatically determined by the software) under "Prior information on linear rate of change." Values between -99% and +1000% are allowed. The program converts these percentages into linear rates of change in natural log space.


Prior information on linear rate of change
Uniform distribution
Min -95 %
Max 400 %
Enter the endpoints of the distribution in terms of percent increase or decrease (between -99% to 1000%)

If users require other distributions of the Bayesian prior, these can be added in future versions of the software.

5) Enter the MCMC specifications to the right of the prior information entry boxes. See details on MCMC specification described in Section 4.2 for **Abundance-based metrics #2: Bayesian analyses**. Default values are provided.

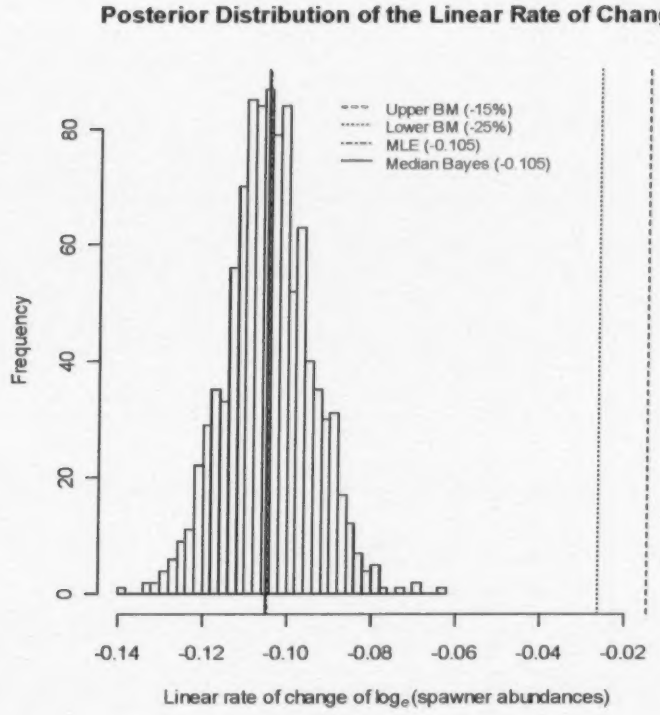
6) To start the Bayesian analysis, click on the "Run MCMC" button. This step will take a few moments. When the iterations are finished, the button will appear to "pop" back up.



7) Select "Generate trace plots of MCMC samples" and proceed through the diagnostic tests for model convergence described in steps (*i*) through (*iii*). Select "Generate autocorrelation plots" and follow the instructions for step (*iv*). See Section 4.2 above for additional instructions and details on MCMC sampling.

8) Once parameter estimates from the Bayesian analyses have converged, proceed to the Results section. To generate a plot of the posterior distribution of short-term trends in abundance, select "Show histogram of the posterior distribution...." The median value calculated for the percent change in the short-term trend, converted to raw percentages, is also shown. Status assessment based on the median of the posterior distribution is shown with an "x" in the appropriate coloured box.

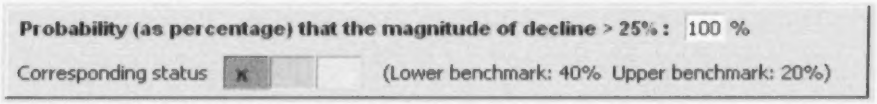
Results
Show histogram of the posterior distribution of linear rates of change.
Median decline or increase of short-term trend:
-68.46 %



The figure above shows a histogram of the posterior distribution of the linear rates of change of smoothed, $\log_e$-transformed spawner abundances. For pink salmon, abundances are $\log_e$-transformed, but not smoothed. The prior distribution used here was the default provided in the GUI, 95% decrease (-0.272 linear rate of change of $\log_e$(spawners)) to 400% increase (0.146 linear rate of change of $\log_e$(spawners)). The maximum likelihood estimation value (solid line) in the plot above is almost indistinguishable from the median (dashed) Bayesian posterior value.

For some combinations of datasets and priors on the uniform distribution, the histogram may be truncated. This is because the MCMC values generated by the program will not exceed the minimum and maximum values that are entered as the mean prior and converted to the corresponding natural logarithm values.

The probability that the magnitude of decline is > 25% is shown with the corresponding status assessment. Provisional lower and upper benchmarks have been chosen at 40% probability and 20% probability of declines of magnitude greater than 25% over the longer of 3 generations and 10 years. The values shown below result from the same dataset as the histogram shown directly above. Note that here, unlike other metrics of abundance, high values of the metric represent increasing management concern and indicated status in the Red zone.


Probability (as percentage) that the magnitude of decline > 25% : 100 %
Corresponding status
(Lower benchmark: 40% Upper benchmark: 20%)

9) Enter any notes in the text entry box to be included in the output summary file. The program will accept multiple lines of notes, with or without hard returns.

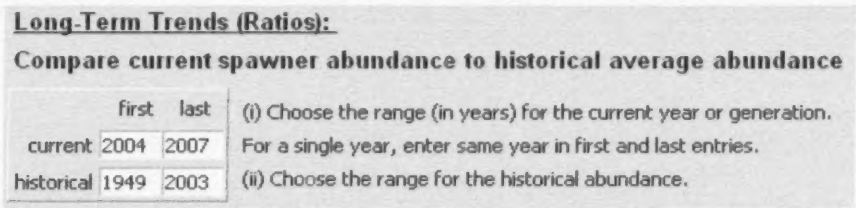
10) Click on "Print summary to file" to generate a text file with all of the inputs and outputs shown on the page. The file will be saved in the working directory, named by the species and CU name that was entered on the **Data** page, and the metric that was summarized. For example, "SE_EarlyStuart_STtrends.txt" is the name of the summary file that summarizes the short-term trend analyses from the **Trend-based metrics #1** page for Sockeye (SE), where "EarlyStuart" was entered as the CU name.

5.2 Long-term trends in spawner abundances

In this section, status on long-term trends in spawner abundances is assessed. Specifically, the ratio of the current abundance to a historical baseline is identified, with lower and upper benchmarks at 0.25 and 0.05, respectively (Holt et al., 2012).

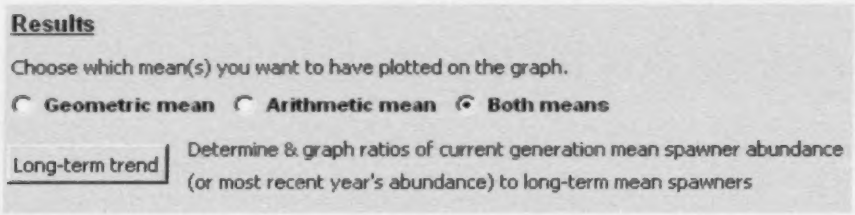
1) Choose the **Trends#2** tab at the top of the GUI window.

2) Enter the first and last years of spawner data to be included in the calculation of current spawner abundances (i.e., the years covering the most recent generation, or only the most recent year). The default is the range covering the last generation as based on the average generation time that was entered on the **Data** page. If the current generation is comprised of a single year (e.g., for pink salmon), enter the same year in both the "first" and "last" columns for this row.

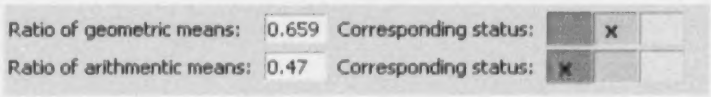


3) Select the range of historical data from which to estimate the historical baseline. Overlaps between the historical and current years are not allowed by the program. The default is all years prior to the last generation. For the ratio calculation, the program allows users to enter a subset of the historical time series that was entered on the **Data** page.

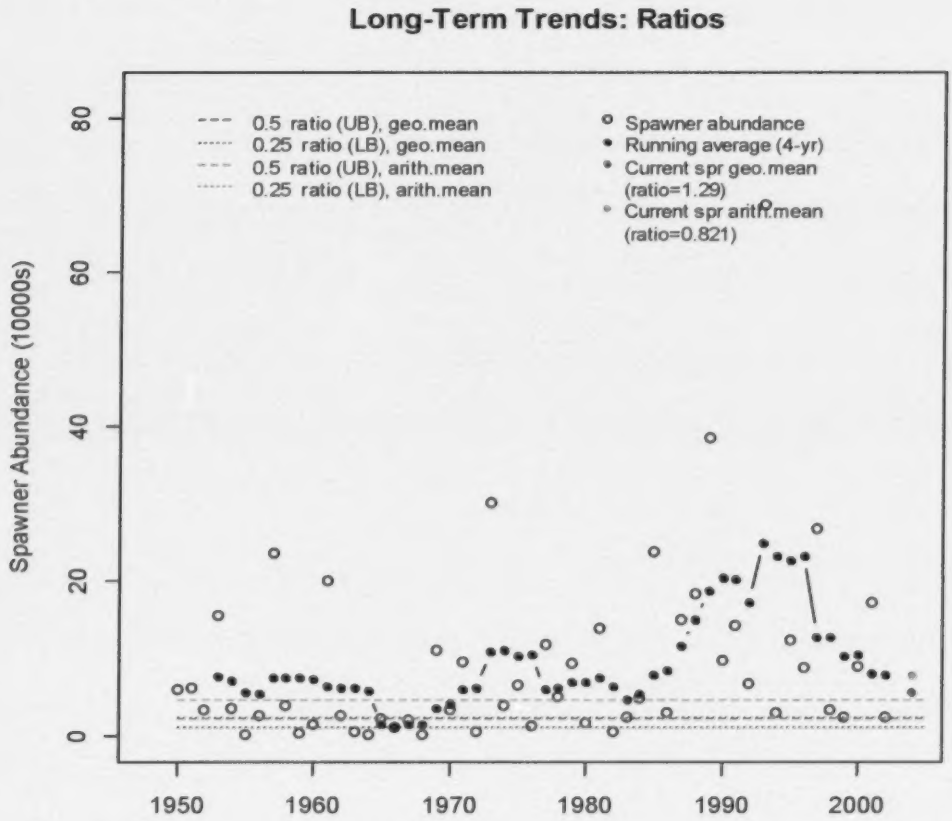
4) Click on the "Long-term trend" button to generate the ratios of means, both geometric and arithmetic, of the recent spawner abundance to the historical baseline. The GUI gives you the option of seeing either or both types of means on the graph.


Results
Choose which mean(s) you want to have plotted on the graph.
Geometric mean
Arithmetic mean
Both means
Long-term trend
Determine & graph ratios of current generation mean spawner abundance
(or most recent year's abundance) to long-term mean spawners

The status corresponding to each ratio will be indicated by an "x" in the coloured boxes to the right of those ratios. The "Long-term trend" button also generates a plot showing the long-term trends in spawner abundance and the ratios of current spawner abundance to the long-term trend.



The lower and upper benchmarks on long-term trends (25% and 50% of the historical mean) are shown on the plot below with dotted and dashed lines, respectively. Benchmarks derived from the geometric mean are shown with blue lines and from the arithmetic mean with red lines. Blue and red points are the geometric and arithmetic means of the current generation, respectively. In the example below, the historical geometric mean spawner abundance is 4.28×10^4 spawners (which is not shown on the plot), 25% of the historical mean is 1.07×10^4 spawners (lower benchmark), and 50% is 2.14×10^4 spawners (upper benchmark). The geometric mean ratio shown in parentheses in the legend on the top right (i.e., 1.29) is the ratio of the geometric mean current spawner abundance (5.52×10^4) to the geometric mean of historical spawner abundance (4.28×10^4). Similarly for the arithmetic mean ratio shown in the plot's legend.



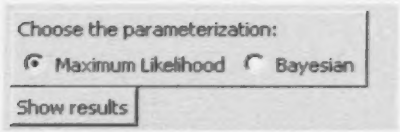
For pink salmon, the most recent year's spawner abundance will be used, rather than the geometric and arithmetic means. However, both the arithmetic and geometric mean historical abundances are calculated for pink salmon, so there will again be separate ratios calculated for the arithmetic and geometric means.

5) Enter any notes in the text entry box to be included in the output summary file.

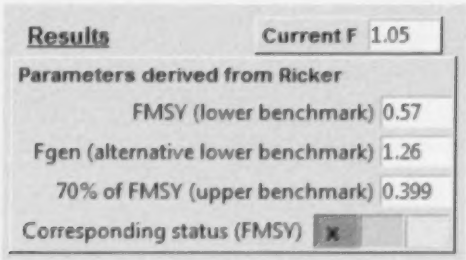
6) Click on "Print summary to file" to generate a text file with all of the inputs and outputs shown on the page. The file will be saved in the working directory, and its name uses the species and CU name that was entered on the **Data** page, as well as the metric that was summarized, e.g., SE_EarlyStuart_LTtrends.txt.

6. Fishing mortality-based metrics

1) Under "SRR-Derived Fishing Mortality," choose the set of Ricker model parameters to be used here (maximum-likelihood or Bayesian) that were estimated in the **Abundance-based metrics** pages.

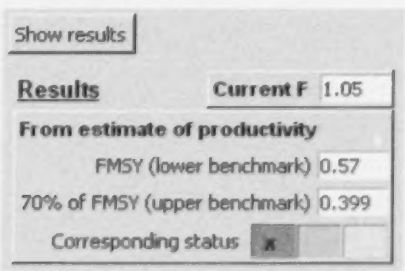


2) Click on "Show results." Note that if you switch between the maximum likelihood and the Bayesian toggles, you will have to click on "Show results" again to load the correct parameters into the software.



The GUI will indicate the corresponding status corresponding to F_{msy} as a lower benchmark and 70% of F_{msy} as an upper benchmark. . Note that unlike most of the metrics of trends and abundance, high values of this metric represent increasing management concern and indicate status in the Red zone.

3) If spawner-recruit data are not sufficient to determine the Ricker parameters, it is also possible to compare fishing mortality to benchmarks from user-derived estimates of stock productivity (e.g., from meta-analyses that use information from neighbouring CUs). This calculation can be made in the box titled "User-Derived Productivity Estimates." If the estimated stock productivity has been entered on the **Data** page, click "Show results." The status will be indicated by an "x" in the coloured boxes at the bottom. Note, F_{gen} requires estimates of carrying capacity and cannot be calculated from productivity alone.



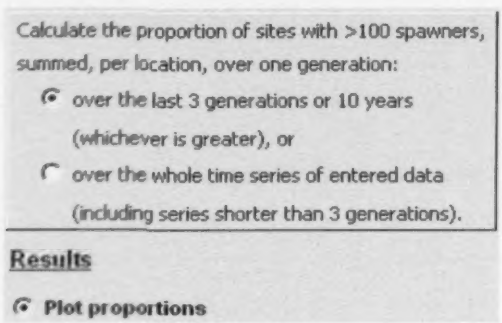
4) Enter any notes to have as part of the output file, and click on "Print summary to file" to generate a text file that records the metrics and benchmarks shown on the page. The file will be saved in the working directory, named by the species and CU name that was entered on the **Data** page, and the metric that was summarized, e.g., SE_EarlyStuart_Mort.txt.

7. Distribution-based metrics

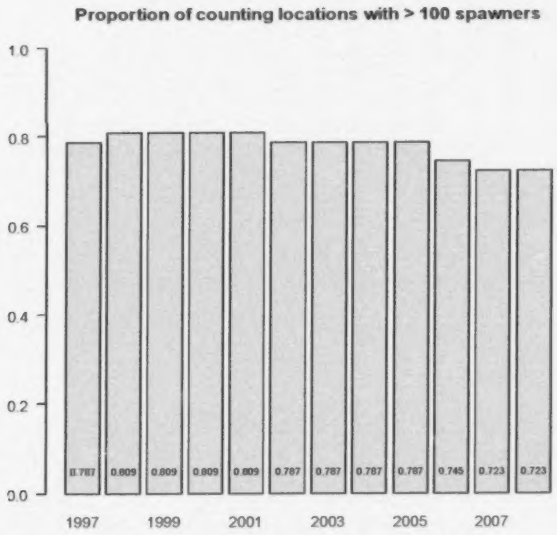
In this section, two metrics of the spatial distribution of spawners are developed. Other metrics are described in Holt et al. (2009), and can be included in future versions of the software. The first metric is the proportion of counting locations that have > 100 spawners when abundances are summed over one generation. Specifically, this metric is calculated in year *t* for the generational sum abundances from year *t*-(generation time-2) to *t*+1. By aggregating abundances over a generation, the net impact of all cycle lines is evaluated at once. The proportion is then plotted over time. The second metric, area over the curve (AOC), reflects the relative contribution of spawners from different counting locations within a CU to total spawner abundances over the CU, and is calculated as a running average over one generation. Increases in AOC over time reflect a concentration of spawners into a smaller number of counting locations within the CU. See Peacock and Holt (2012) for a more detailed description of this metric. Benchmarks have not yet been identified for **distribution-based** metrics.

Distribution metrics should be interpreted with caution because of non-systematic sampling, both spatially and temporally, especially of smaller populations (Holtby, *in review*). Furthermore, there are a variety of possible interpretations of entries of zero for a counting location (e.g., missing data or zero fish observed when fish were expected) (Holtby, *in review*).

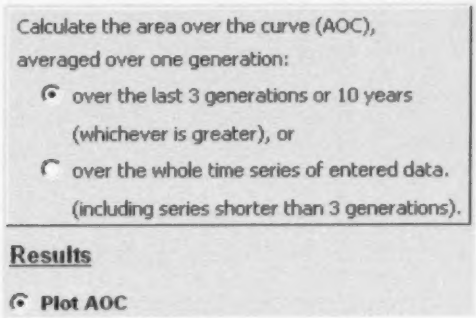
1) In the "Proportion of Sites with >100 Spawners" section, choose whether to generate a plot from the dataset as entered, or the greater of the last 3 generations or 10 years. For pink salmon, the last 10 years will be represented by 5 spawner returns. If the time series of the dataset is too short to graph the last 3 generations or 10 years, select the "over the whole time series of entered data" option. That option can also be selected if it is desirable to view more than 3 generations of distribution data.


Calculate the proportion of sites with >100 spawners, summed, per location, over one generation:
over the last 3 generations or 10 years (whichever is greater), or
over the whole time series of entered data (including series shorter than 3 generations).
Results
Plot proportions

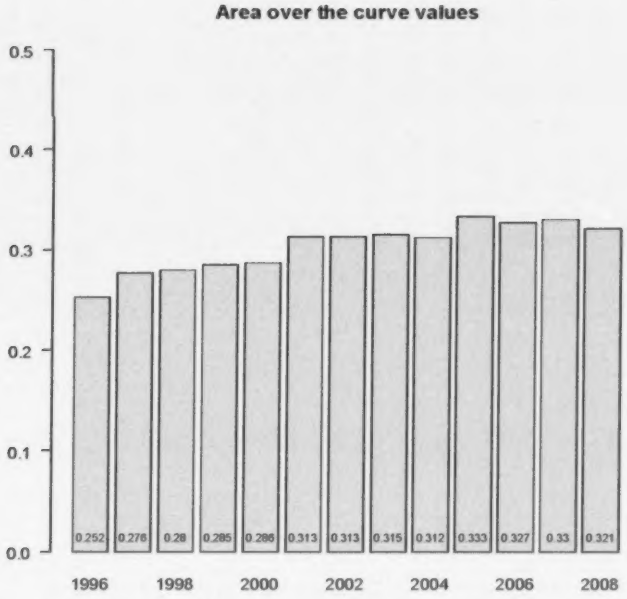
2) Select "Plot proportions" to show the time series of proportions. When time-series are relatively short (<15 years), the metric values are printed on individual bars of the plot. These values are omitted on plots of longer time-series.



3) In the box titled "Area Over the Curve," again select whether to use the whole time series of data or the most recent subset of 3 generations or 10 years. AOC in year *t* is calculated for the generational sum abundances from year *t*-(generation time-2) to *t*+1.


Calculate the area over the curve (AOC),
averaged over one generation:
over the last 3 generations or 10 years
(whichever is greater), or
over the whole time series of entered data.
(including series shorter than 3 generations).
Results
Plot AOC

4) Choose "Plot AOC" to graph the time series of AOC values.



5) Enter any notes in the text entry box to be included in the output summary file.

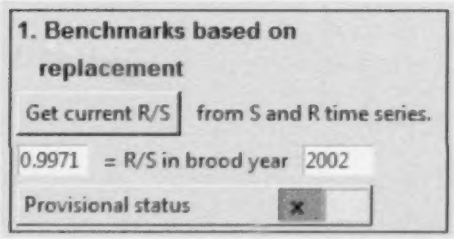
6) Click on "Print summary to file" to generate a text file that shows the calculated values that were plotted in the graphs. The file will be saved in the working directory, named by the species and CU name that was entered on the **Data** page, and the metric that was summarized, e.g., SE_EarlyStuart_Distr.txt.

8. Productivity-based metrics

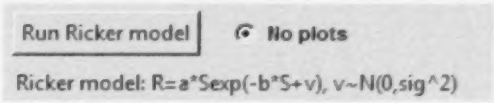
In this section, status is assessed based on current productivity and trends in productivity. The benchmarks determined here are provisional and were derived from (Grant and Pestal *in press*) and Holtby (*in review*).

(1) To determine status based on recruits per spanwer, first enter the spawner and recruit time series on the **Data** page under "Abundance-Based Metrics."

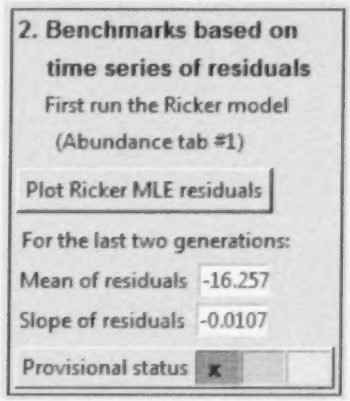
(2) On the **Productivity-based metrics** page, click "Get current R/S," which will calculate recruits per spawner in the most recent brood year for the file entered in the S-R time series on the **Data** page. That ratio will be compared to the replacement level of recruits/spawner (=1) which was suggested as a lower benchmark in Holt (2012). No upper benchmark has been provided.



(3) To determine status based on residuals from the stock-recruitment relationship, first enter S-R data on the **Data** page and run the Ricker model on the **Abundance#1** page.



(4) On the **Productivity** page, click on "Plot Ricker MLE residuals" to determine status based on provisional benchmarks.



Provisional benchmarks based on the time series of residuals were assessed by determining the mean and slope of residuals according the maximum likelihood estimation of the Ricker function over (provisionally) the last two generations. If both the mean and the slope are negative, the corresponding status zone is Red. If only the mean or slope is negative, the status is Amber. If both are positive, the status is Green.

(5) Enter any notes in the text entry box to be included in the output summary file. The program will accept multiple lines of notes, with or without hard returns.

(6) Click on "Print summary to file" to generate a text file with all of the inputs and outputs shown on the page. The file will be saved in the working directory, named by the species and CU name that was entered on the **Data** page, and the metric that was summarized, as detailed at the end of section 4.1. E.g., SE_EarlyStuart_Prod.txt.

9. ACKNOWLEDGMENTS

Thank you to S. Grant, M. Thiess, E. Porszt, B. MacDonald, and P. Hall for providing valuable feedback in the development of the software and documentation

10. LITERATURE CITED

Note that some of the references listed here are available from the "References" or "Help" drop-down menus at the top of the CU Metrics and Benchmarks GUI, and others may become available when final versions of those documents have been prepared or published.

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